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Press release

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## **A major advance in plant biology: the grapevine genome is completely sequenced**

**A major achievement has been reached in plant biology: the first detailed analysis of the grapevine genome has just been published. The joint effort carried out by scientists from Genoscope and INRA in France and from several Universities and the Istituto di Genomica Applicata (IGA) in Italy has produced a high-quality draft of the genome sequence of *Vitis vinifera*, the first for a fruit crop, cultivated for both fruit and beverage. The results of this analysis allow a better understanding of plant evolution and genes involved in wine aromas. The details are published in the online Nature paper of August 26th 2007.**

The grapevine joins the other three plant species sequenced so far: thale cress (*Arabidopsis thaliana*), rice and poplar. The project aiming at the characterization of the grapevine genome was launched in 2005 within a scientific cooperation agreement between the Ministry of Agriculture in France and the Ministry of Agriculture in Italy. It is coordinated by INRA and Genoscope in France and by CRA in Italy.

The public release of the grapevine sequence is both a fundamental accomplishment and a starting point for a deeper characterization of gene function. This is crucial for a better assessment of natural variation and its relevance to phenotypic variability, and the realization of applicative projects, aimed for instance at the development of grapevine resistant to diseases. This in turn will contribute to the much-needed reduction of fungicide and pesticide treatments and the development of a more sustainable agriculture.

The inbred line selected for the project, derived from Pinot Noir, was obtained at the INRA Research Centre of Colmar. The choice of this line allowed the French-Italian public consortium to obtain a very high quality sequence of approximately 480 million base-pairs, which unveiled some of the secrets of the constitution of the grapevine genome. The sequencing operation began in December 2005. Genoscope (Paris, France), IGA (Udine, Italy) and CRIBI (Padova, Italy) produced more than 6 million short genome fragments and the resources and expertise of all the partners (including Genoscope and INRA for France) were mobilized to analyse the sequence obtained.

### **Major results to understand the evolution of flowering plants**

The comparative analysis of the grapevine genome and those of rice, poplar and *Arabidopsis*, has revealed the ancestral nature of the grapevine genome in comparison to the other plant species and

has allowed researchers to get a glimpse of how a plant genome looked like in the progenitor of flowering plants.

### ***Towards a better understanding of aromas in wines***

A striking feature of the grapevine gene content is the existence of large families of genes related to wine flavour, which have a very high gene copy number. This is the case, for instance, for the genes coding for stilbene synthase, an enzyme which drives the synthesis of resveratrol, the compound responsible for the health benefits associated to a moderate consumption of wine. A similar situation is found for genes coding for enzymes involved in the synthesis of terpenes and tannins, the major components of aromas, resins and essential oils.

The grapevine sequence is fully accessible to the world scientific community through public databases. The French-Italian public consortium has been offering complete access to its sequencing results since October 2006 through three public websites\* whose browsers are intensively accessed by scientists worldwide.

This project was financed by the French Ministry of Higher Education and Research, the Consortium National de Recherche en Génomique, the Agence Nationale de la Recherche, INRA, the Italian Ministry of Agriculture (VIGNA-CRA), and Regione Autonoma Friuli Venezia Giulia together with a consortium of private companies and banks (IGA).

\*The French-Italian public consortium has been offering complete access to its sequencing results since October 2006 through three public websites: <http://www.genoscope.cns.fr/vitis>, <http://www.vitisgenome.it/> and <http://www.appliedgenomics.org>

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**"The grapevine genome sequence suggests ancestral hexaploidization in major agiosperm phyla"**  
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<http://www.nature.com/nature/journal/vaop/ncurrent/index.html>

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